

1	400	34.1	2032	4	US-09-045-284A-1	Sequence 1, Appl
2	235.2	20.1	2156	2	US-08-899-514-1	Sequence 1, Appl
3	196.8	16.8	2354	1	US-08-665-878-1	Sequence 1, Appl
4	148.8	12.7	2409	3	US-09-263-023-3	Sequence 3, Appl
5	133	11.3	2150	3	US-09-263-023-3	Sequence 1, Appl
6	64.6	5.5	43280	2	US-08-604-227C-1	Sequence 1, Appl
7	57.8	4.9	731	4	US-09-040-984-63	Sequence 63, App
8	57.2	4.9	30001	1	US-08-125-468-1	Sequence 1, Appl
9	57.2	4.9	30001	2	US-08-174-933-1	Sequence 1, Appl
10	55.6	4.7	1931	2	US-09-130-114-2	Sequence 2, Appl
11	54.6	4.7	4689	4	US-09-105-537-34	Sequence 34, Appl
12	54.6	4.7	36778	4	US-09-120-878-19	Sequence 5, Appl
13	54.6	4.7	38506	3	US-09-320-878-19	Sequence 19, Appl
14	52.8	4.5	2580	3	US-09-050-863-2	Sequence 2, Appl
15	52.8	4.5	5452	2	US-09-130-114-1	Sequence 1, Appl
16	52.8	4.5	9600	4	US-08-910-647-1	Sequence 1, Appl
17	52.8	4.5	10596	1	US-07-884-811-15	Sequence 15, Appl
18	52.8	4.5	10596	1	US-07-885-971-15	Sequence 15, Appl
19	52.8	4.5	10596	1	US-08-087-783A-15	Sequence 15, Appl
20	52.8	4.5	10596	1	US-08-194-088B-15	Sequence 15, Appl
21	52.8	4.5	10596	2	US-08-194-087-15	Sequence 15, Appl
22	52.8	4.5	10596	2	US-08-194-087-15	Sequence 15, Appl
23	52	4.4	4897	6	PCN-US93-046A-8-15	Sequence 15, Appl
24	50.4	4.3	674	3	US-09-066-811-1	Sequence 1, Appl
25	50.4	4.3	674	4	US-09-543-106-1	Sequence 1, Appl
26	50.4	4.3	1734	6	5352575-8	Patent No. 5352575
27	50.2	4.3	2846	4	US-09-613-182-5	Sequence 5, Appl

602 atccacacagatgaaatcattccccggyctcaatgtcagcgtccgtgtgcaagtcacacagccc 661

```

? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: DANIEL E ALTMAN
? REGISTRATION NUMBER: 34,115
? REFERENCE/DOCKET NUMBER: TOYAM21.001AUS
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 714 760 0404
? TELEFAX: 714 760 9502
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 2156
? TYPE: nucleic acid
? STRANDEDNESS: both
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? ORGANISM: Human
? TISSUE TYPE: Fetal brain
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 147..1583
? IDENTIFICATION METHOD: S
?
? US-08-899-514-1
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Query Match          20.1%; Score 235.2; DB 2; Length 2156;
Best Local Similarity 54.0%; Pred. No. 7,4e-41;
Matches 589; Conservative 0; Mismatches 468; Indels 33; Gaps
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Oy      91 gggccctacaccagccgagcgcgagagatcgtgtgcacgtgcgtggttcctcgttg 150
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Db      510 GAGCCGCCGAGACCGGGCCTGTGGCGGGGCCCGCGGCATGTCGTATATGCCACCAG 569
?
Oy      151 cgctcgagctatccttctttgtgccagctcttcagcaaacccgaagcttctaactg 210
       ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      570 CGAGCGGGCTCCTCTTCTGTGGGCGAGTTCTTCAACAGCACAGGGAACATCTTCACCTC 629
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Oy      211 atgagagccgcgtaggatgtgtggaaccacctgtc-----gcaggagcagcgcg 258
       ||||| | | | | | | | | | | | | | | | | | | | | | | | |
Db      630 TTCCAGCGCTGTGGCATCATCAGCGGCACAGTGTCCTTCAGCCGGGGGGCCCAAGCGC 689
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Oy      259 gcaacgctcacatgtgcgtgtgcgcgacacttgatgctcatcttlttgtgagacaatgac 318
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Db      690 GCGGGCTCGGCCCTCGGTACTCCGCGAGCTGCTCAACAGACTCTTCCTGTGCACTGTAC 749
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Oy      319 gtgtttgatgacctaca-----tgcaacagagcgaaacctgtgcgccttlttcaac 369
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Db      750 GTGCTGGAGGACATTATCATCAGCGCGCTGCCGAGGACCACTGACTCAAGTTCATGTTCCGC 809
?
Oy      370 tgggcaacagccgcgcgtctgtgtctgcgcgcgcgcctgtcagcgaccttcccagagcaac 429
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Db      810 CGGGGCTTCACACCGCTCCCTGTGCGAGAGACCCCTCTGTACGCCCTTCGTCAAGAAGTTC 869
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Oy      430 atcaagaagcagagagtataagaagacactgtgcgcgcgcagaccattcagccctggccccg 489
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Db      870 TTCGAAAGATACACTGCAAGAACCGCGCTGCGGCCCTCCAACGTGAGCGTAGGCCGA 929
?
Oy      490 gagcgctgcgcgtctctacagcaacgltgttctaagaagatgftgccttccaacctgtcag 549
       ||||| | | | | | | | | | | | | | | | | | | | | | | |
Db      930 GAGGCTTGCGCGCGAGAGACATATGCGCTTCAAAGGCGGTGCCATTCGGGACACTGGAG 989
?
Oy      550 gtgtcttacacgctgtcctcagcgaaacccgcgcctcaacctgcgcatalgtgtacactgtgcgc 609
       ||| | | | | | | | | | | | | | | | | | | | | | | | | |
Db      990 TTCCTCAGACCCCTGTGCTGAGAGACCCCGCCTGGACACTGCCGTATACACTGTGTGGC 1049
?
Oy      610 gaccgcgagcggtgtgtgtgtgtcccggaagcgcgagccgatactgtgcaagcgagaac 669
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Db      1050 GACCCCCGGGCGCTGTGGCTGTGCGCAGAGTGTGGCTTCGCCGCAATATTAAGACCTGG 1109
?
Oy      670 ggaatcgtgtgtgtgcaaccaagtgaggtgtgtgagccgaaccttaactgtgcctgaatt 729
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Db      1110 AAGAGTGGCTTGAGACGACGAGGGCCAGGAGCGCTGTAGGGAAGAGAGGTGACGGCTG 1169

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QY 730 cgcagagtggtccgcaagcagctgcatcgccgaggccgccaactcaagccgcaacc 789
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Db 1170 CGGGGCAACTGCGAGAG---CATCCGCTCTCCGCGAGCTGGGGCTGGCGACGCCGCC 1226
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 790 ttcctgcgcgcgcgtacccgctggtgctgctgagagcctggcgaggcgctgga 849
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1227 TGGCTGCGGGCGCTACATGCTGTGCGCTAGAGAGACTGGCACCGGGCGCTGCGAG 1286
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 850 gaatccgcgcacttaagccttcacccgagcctgaacctcaaccgcaagcctgagccttg 909
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1287 AAGGCCGCGAGATGATACCGCTTCCGCGGATCCCTGTAGCCCGGAGGGAAGACTGG 1346
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 910 atccacacatcacccagcggtgcggagatcggaagccaactcgagccttcaacttcg 969
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1347 ATCCAAAAGAACACGACGCGGCGCCACGACGCGCA-----GCGGCAATCTACTCCAG 1397
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 970 tctaggaatgcgcgaacgctcccgagcctgagcgcagcgcttgccctcaatgaatc 1029
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1398 CAGAGAACTCCTCGAGAGAGTTCGAGAGAGTGGCGCTTCAGCATGCCCTTCAAGCTGCGC 1457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1030 ctgcgcgtgcagagagtgctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1089
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1458 CAGGTGTGCAAGGCCCGCGCGCGCTGCATGCGCTTTCGCTACAACTGGCGCGG 1517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1090 tctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 1149
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1518 GACGCGCGCGCTCACCACCGCTCAGTCAAGCTGCTGAGGAGAGGCGGCACTTCTGG 1577
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1150 ttcagctggg 1159
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1578 GTCACGTAGG 1587
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RESULT 3

US-08-655-878-1

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; Sequence 1, Application US/08655878
; Patent No. 5827713
; GENERAL INFORMATION:
; APPLICANT: FUKUTA, MASAKAZU
; APPLICANT: HABUCHI, OSAMI
; TITLE OF INVENTION: DNA CODING FOR SULFOTRANSFERASE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:
; STREET:
; CITY:
; STATE:
; COUNTRY:
; ZIP:
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/655, 878
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME:
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2354
; TYPE: nucleic acid
; STRANDEDNESS: both

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; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Chick
; TISSUE TYPE: Embryo chondrocyte
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 211..1584
; IDENTIFICATION METHOD: P
;
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 211..309
; IDENTIFICATION METHOD: P
;
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 310..1584
; IDENTIFICATION METHOD: P
;
; FEATURE:
; NAME/KEY: transmembrane domain
; LOCATION: 280..321
; IDENTIFICATION METHOD: P
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 280..402
; IDENTIFICATION METHOD: S
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 427..435
; IDENTIFICATION METHOD: S
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 493..501
; IDENTIFICATION METHOD: S
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 916..924
; IDENTIFICATION METHOD: S
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 1405..1413
; IDENTIFICATION METHOD: S
;
; FEATURE:
; NAME/KEY: potential N-glycosylation site
; LOCATION: 1537..1545
; IDENTIFICATION METHOD: S
;
; US-08-655-878-1
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; Query Match
; Best Local Similarity 16.8%; Score 196.8; DB 1; Length 2354;
; Matches 575; Conservative 0; Mismatches 487; Indels 36; Gaps 5;

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QY 52 cagaccactgctctctctctcaatcattcccgagcgccctatcccgagcgcg 111
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Db 475 CTGAGAGCGCGGCTCGCAACGACCTTGCATTTGGTGGGAGCTGGGCAATAGAGCC 534
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 112 ggcgagatcggtgacgtgctgctgctgctgctgctgctgctgctgctgctgctgctg 171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 535 CCAGAGCGCGGCGGCTATCTCTGATGATGCGCACACGACGCGGCTCTCTCTCTGTT 594
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QY 172 ggcagctcttcagccagcccgagcgctcttactactgagagcccgctggaatgctg 231
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Db 595 GGGAGATTCTTAACCAAGAGGCAACATATTCTTACCTTTGAGGCCCTGTGGCACATC 654
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QY 232 tgaccacacctgtc-----gcaggcgagcgcggaacgctgcaactgagcgctg 279
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Db 655 GAGAGAGCGGTCATTTGAGCGAGGGGGGCGCAACGCGGTGGCTGGGCTCTGTGTAC 714
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QY 280 cgcgacgtgagcgtctatcttttgcgagacatgagcgtgttgatgacatgacga 339
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Db 715 CGGACGTGTGACAGACACTCTCTCTGCGACGCTTACATTTCTGAGAGCTTCTATCTCA 774
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QY 340 cagagcggaacctgtc-----gccttttaacttgcggaacgagcgcgctg 390
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[illegible]

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NAME/KEY: CDS
LOCATION: 20010..31199
FEATURE:
NAME/KEY: CDS
LOCATION: 31232..36067
FEATURE:
NAME/KEY: CDS
LOCATION: 36249..41774
US-08-804-227C-1

Query Match 5.58; Score 64.6; DB 2; Length 43280;
Best Local Similarity 44.7%; Pred. No. 4.4e-05;
Matches 305; Conservative 0; Mismatches 369; Indels 9; Gaps 1;

QY 396 gccgcccgtgcaagcccttcccgagccacatcagaagaagagcgtatcgagac 455
DB 29720 GCCGCTACCGCTACCGCATACGCGACGCCGCCGCCCTTGGCCACCTCAGCAGGC 29779
QY 456 acgtgcaagcagcagcattcagccctgcccggagcctgcgcctcctacaagcagt 515
DB 29780 CCGGACACCGGCAAGCTGCTGCTGACGGGTGCTGCGCGGATTCAGACACCAGCGGT 29839
QY 516 ggtgctcaagagagtgctcttcaacctgcaagtgctctacccgctgctcagcgacc 575
DB 29840 GCTCTACCGCGGCGACCGGCGACGCTCGGCGACAGACATCGCCCGCATCTGTCACAC- 29898
QY 576 cgcgctcaacctgcgaatcgatcgactggtgcgagccgcggcgctgctgcctccg 635
DB 29899 -----GCCACGGCGTACGCGACCTGCTCGCGCGCGCACCGCGCGCGCGCGA 29950
QY 636 ggaagcgagcgagccgatactgcaagcgagcaagcgatcgctggtggaaccaagcgaa 695
DB 29951 GGGCGTCCGCGAACCTGATTGTAACCTGGGCGAGTTGGCGCGCGGCTCGCGGCGC 30010
QY 696 gtgggtgagcgagccagcctcagctgagctgagtgctgcgcagcgagcgagcg 755
DB 30011 CTGGGACGCGCGCGGCGGCGGCGCTCACCGGAACTCTGCGCGGAATCCCGCTGAGCA 30070
QY 756 catcgccgagcgagccagcactcaagccgacacccctctgcgcgcgcgtacgcgtg 815
DB 30071 CCGGCTCGGCGCGCTGCTCCACGCGCGGCGGCGACCTCGAGACGCGACCATCCCTCACT 30130
QY 816 ggcgttcgaggaactgagcgagcgagcgctgagagatcgcgagcactctacgccttac 875
DB 30131 GACCGGCGGAGACATGACAAACGTCGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30190
QY 876 cgcgctgagccctcaagcagcagctgagcgctgagatccacaacacccaagcggtcg 935
DB 30191 CGAGCTGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCT 30250
QY 936 gatcggaagcgaatcgagcgcttccactgctctagaatgagcgagcgagctccca 995
DB 30251 GCTCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30310
QY 996 ggcgtgagcgagcgagcgctgagccttcaatgagatcgagcgagcgagcgagcg 1055
DB 30311 CCGATACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30370
QY 1056 cgcgctgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgagcgag 1078
DB 30371 CAACAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 30933

RESULT 7
US-09-040-984-63
Sequence 63, Application US/09040984
Patent No. 6210883
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Wang, TongTong
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS

TITLE OF INVENTION: OF LUNG CANCER
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/040,984
FILING DATE: 18-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mark I. David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.456
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-622-4900
TELEFAX: 206-282-6031
TELEX:
INFORMATION FOR SEQ. ID NO: 63:
SEQUENCE CHARACTERISTICS:
LENGTH: 731 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-040-984-63

Query Match 4.98; Score 57.8; DB 4; Length 731;
Best Local Similarity 58.4%; Pred. No. 0.00061;
Matches 101; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 515 tgggtctcaagagagtgctcttcaacctgcaagtgctctacccgctgctcagcgac 574
DB 3 TAGTCATTAAGGAGTGCTCGCGCTTCACACGTCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 62
QY 575 cgcgctcaacctgcgactgctgactggtgagcgagccgcggcgctgctgagcacc 634
DB 63 CGGCGCTGAGCCTCAAGCTATCCATTCGCTGATCCCGCGGCGGCGGCGGCGGCGGCGGCGG 122
QY 635 gggagggcgagcccgatactgagcgagcgagcgagcgagcgagcgagcgagcgag 687
DB 123 GGATCCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 175

RESULT 8
US-08-125-468-1/C
Sequence 1, Application US/08125468
Patent No. 5589385
GENERAL INFORMATION:
APPLICANT: Ryan, Michael J.
APPLICANT: Lotvin, Jason A.
APPLICANT: Strathy, Nancy
APPLICANT: Fanti, Susan E.
TITLE OF INVENTION: Cloning of the biosynthetic pathway for
TITLE OF INVENTION: chlorotetracycline and tetracycline formation and cosmi
TITLE OF INVENTION: useful therein
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: American Cyanamid Company
STREET: One Cyanamid Plaza
CITY: Wayne
STATE: New Jersey
COUNTRY: USA
ZIP: 07470
COMPUTER READABLE FORM:


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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1931
; TYPE: DNA
; ORGANISM: EBNA
US-09-130-114-2

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Query Match      4.7%; Score 55.6; DB 2; Length 1931;
Best Local Similarity 44.7%; Pred. No. 0.0021;
Matches 217; Conservative 0; Mismatches 269; Indels 0; Gaps 0;

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QY 476 tcagctggcccggaagctgacgtctcctacagccagcgggtgtcctaaggaggtgagct 535
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DB 450 tctctctcccgctcccgctcctcgtctcctcctcccgctcccgctcccgctcccgctcc 509
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 536 tctcaacgtgagctgtctacccgctgtcagcgaacccgacccgacccgacccgacccg 595
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DB 510 tctgtctctcccgctcctcgtctcctcctcccgctcccgctcccgctcctcctcccg 569
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    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 570 tctctcccgctcctcccgctcctcgtctcctcctcccgctcctcctcctcccgctcc 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 656 tggcagcgagacagcagctgtctggtgacacagcggaagtggtggaagcgacccctc 715
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 630 tctctcccgctcctcctcctcccgctcctcctcccgctcctcctcccgctcctcccg 689
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QY 716 acctgagcgtgattcgcgaggtgtgcgcgacgacgagcgatcgccgagcgccgaac 775
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 690 tctctgctcctcccgctcctcgtcctcccgctcctcctcccgctcctcctcctcccg 749
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 776 tcaagcgcgcacccctctgagcgagcgctacgacgctgtgctgctcagagacgtgagc 835
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 750 tctctcccgctcctcctcccgctcctcctcccgctcctcctcccgctcctcctcccg 809
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 836 gggagcgctgagcagagatccgcgacactctacgctctacacgctgacccctcagccac 895
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 810 tctgtctcctcccgctcctcctcccgctcctcctcccgctcctcctcccgctcctcc 869
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 896 agctcgagcgctgtatccacaacatcacccagcggtcgaggatcggaacgaatcgagg 955
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 870 tcccgctcctcccgctcctcctcctcccgctcctcccgctcctcctcctcccgctcc 929
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 956 cctctcc 961
    ||| |||
DB 930 ccgtcc 935
    ||| |||

```

```

RESULT 11
US-09-105-537-34
; Sequence 34, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 4689
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-34

```

```

Query Match      4.7%; Score 54.6; DB 4; Length 4689;
Best Local Similarity 44.2%; Pred. No. 0.0038;

```

```

Matches 225; Conservative 0; Mismatches 284; Indels 0; Gaps 0;

```

```

QY 582 caactctgcacatctgtacacctgtgtcgcgaacccgagcgctgtcgtcctcccggaagc 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3408 ccaccacggagcgaacacactctctcctcgttaagccgacgagcggaacaaagcccgagc 3467
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 642 ggcgggcccgaatactgtgcacgagcgaacgagcagctgtcgtggaacccaaggaagtgt 701
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3468 caccacactcaacccgcgaactcaccgacatcggtggcccgctcaacacatcgccgtcgga 3527
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 702 ggaaggccgaacctcaactgtcgtgatctgcgaggtgtgtccgcagccagctgtcgtatgc 761
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3528 cgtcgcgacccccaacgacatcgacacactcctcctcgaacccatcccgccgagagccct 3587
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 762 cgaagccgcacacatcaagccgcgaacctctcgtcgtgagccgtcgaacccgtgtgtgt 821
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3588 caccgcgctgtctcaacacccgcggcgacccggcgagcgtacatcgctggaacgacccgc 3647
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 822 cgaaggaacctgacggggaagcgcgtcgtgcagagatccgcgaactctacagctcaacggact 881
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3648 ggaaggacatccgcccgaatcctgtggtgcgaagacgaagcgcgagctcctcgaacact 3707
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 882 gacctcaacgacacagctcgaagcgtgtgataccaacacatcaacccaggttcggggtatcg 941
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3708 gctccgcggacatccgctgtgagcgtctgtctctactcctcgaacgagcggtgtcggtg 3767
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 942 caagccaatcgagggccttcatactcgtctcgaagaatgctgcgaacgctcctccaggtctg 1001
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3768 cagcgagcagcgaaggggtctactgcgcgcgacgaacccacactcgaacgctcgcgcgcg 3827
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1002 ggcgcagcgttgcctcctaagatctcgtcgtgtcaggaagtgtgtcgcgcgcgcgt 1061
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3828 ggcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 3887
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1062 gcaatgtgtgtgtacacggcgtgtgtact 1090
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 3888 catggcgcgggcgcgacgaacgacgtact 3916
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

```

RESULT 12
US-09-105-537-5
; Sequence 5, Application US/09105537A
; Patent No. 6265202
; GENERAL INFORMATION:
; APPLICANT: Sherman, D.H.
; APPLICANT: Liu, H.
; APPLICANT: Xue, Y.
; APPLICANT: Zhao, L.
; TITLE OF INVENTION: DNA encoding methymycin and pikromycin
; FILE REFERENCE: 600.438US1
; CURRENT APPLICATION NUMBER: US/09/105,537A
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 36778
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
US-09-105-537-5

```

```

Query Match      4.7%; Score 54.6; DB 4; Length 36778;
Best Local Similarity 44.2%; Pred. No. 0.0052;
Matches 225; Conservative 0; Mismatches 284; Indels 0; Gaps 0;

```

```

QY 582 caactctgcacatctgtacacctgtgtcgcgaacccgagcgctgtcgtcctcccggaagc 641
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 30398 ccaccacggagcgaacacactctctcctcgttaagccgacgagcggaacaaagcccgagc 30457
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 642 ggcgggcccgaatactgtgcacgagcgaacgagcagctgtcgtgacccaacggaagtgt 701
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 30458 caccacactcaacccgcgaactcaccgcatggggcgcccgctacacatcgccgctgtgga 30517
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```


[illegible]

```

; RESULT 13
; US-09-320-878-19
; Sequence 19, Application US/09320878A
; Patent No. 6117659
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, Gary
; APPLICANT: BETLACH, Melanie C.
; APPLICANT: BETLACH, Mary C.
; APPLICANT: MCDANIEL, Robert
; APPLICANT: TANG, Li
; TITLE OF INVENTION: RECOMBINANT NARBONOLIDE POLYKETIDE SYNTHASE
; FILE REFERENCE: 300622002120
; CURRENT APPLICATION NUMBER: US/09/320,878A
; CURRENT FILING DATE: 1999-05-27
; EARLIER APPLICATION NUMBER: CIP OF 09/141,908
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: CIP OF 09/073,538
; EARLIER FILING DATE: 1998-05-06
; EARLIER APPLICATION NUMBER: CIP OF 08/846,247
; EARLIER FILING DATE: 1997-04-30
; EARLIER APPLICATION NUMBER: 60/119,139
; EARLIER FILING DATE: 1999-02-08
; EARLIER APPLICATION NUMBER: 60/100,880
; EARLIER FILING DATE: 1998-09-22
; EARLIER APPLICATION NUMBER: 60/087,080
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 38506
; TYPE: DNA
; ORGANISM: Streptomyces venezuelae
; US-09-320-878-19

```

	Query Match	Best Local Similarity	Score 54.6	DB 3	length 38506
	Matches 225; Conservative	44.2%	Pred. No. 0.0033	Mismatches 284; Indels 0; Gaps 0	
QY	582	caactgtgcgcatgtgacacatgtgtgagagaccggcgagcgtgctgcgtctcccggaagc	641		
Db	28540	ccactcagagacgcgaacacatctctctctgcgcgcgcgaacgacacgaaccccccgagac	28599		
QY	642	gagcgagcccgatactgtgcacgcgcgaacacggaactcgtgtcgtggaacacagcaatggagt	701		

[illegible]

```

RESULT 14
US-09-050-863-2/C
; Sequence 2, Application US/09050863
; Patent No. 6114111
GENERAL INFORMATION:
APPLICANT: Lao, Ying
APPLICANT: Hiang, Betty
APPLICANT: Payan, Don
TITLE OF INVENTION: Mammalian Protein Interaction Cloning
TITLE OF INVENTION: System
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/050,863
FILING DATE: 30-MAR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-663638/DJB/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1898
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2580 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA

```

